RAW SEQUENCE LISTING ERROR REPORT
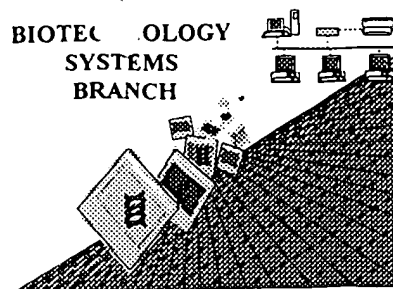
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____09/910,186_____

Source: _____OIPE_____

Date Processed by STIC: _____08/06/2001_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

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RAW SEQUENCE LISTING   DATE: 08/06/2001
PATENT APPLICATION: US/09/910,186   TIME: 15:39:04

Input Set : A:\A33626Aseqlist.txt
Output Set: N:\CRF3\08062001\I910186.raw

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 1 <110> APPLICANT: U.S. Army Medical Research & Material Command
 4 <120> TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
 5       NEUROTOXIN
 7 <130> FILE REFERENCE: A33626-A 067252.0107
 9 <140> CURRENT APPLICATION NUMBER: US/09/910,186
 9 <141> CURRENT FILING DATE: 2001-07-20
 9 <150> PRIOR APPLICATION NUMBER: PCT/US00/12890
10 <151> PRIOR FILING DATE: 2000-05-12
12 <150> PRIOR APPLICATION NUMBER: 09/611,419
13 <151> PRIOR FILING DATE: 2000-07-06
15 <150> PRIOR APPLICATION NUMBER: 60/133,865
16 <151> PRIOR FILING DATE: 1999-05-12
18 <150> PRIOR APPLICATION NUMBER: 60/133,866
19 <151> PRIOR FILING DATE: 1999-05-12
21 <150> PRIOR APPLICATION NUMBER: 60/133,867
22 <151> PRIOR FILING DATE: 1999-05-12
24 <150> PRIOR APPLICATION NUMBER: 60/133,868
25 <151> PRIOR FILING DATE: 1999-05-12
27 <150> PRIOR APPLICATION NUMBER: 60/133,869
28 <151> PRIOR FILING DATE: 1999-05-12
30 <150> PRIOR APPLICATION NUMBER: 60/133,873
31 <151> PRIOR FILING DATE: 1999-05-12
33 <150> PRIOR APPLICATION NUMBER: 08/123,975
34 <151> PRIOR FILING DATE: 1993-09-21
36 <160> NUMBER OF SEQ ID NOS: 34
38 <170> SOFTWARE: FastSEQ for Windows Version 4.0
40 <210> SEQ ID NO: 1
41 <211> LENGTH: 1332
42 <212> TYPE: DNA
43 <213> ORGANISM: Synthetic Construct
45 <220> FEATURE:
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (13)...(1326)
51 <400> SEQUENCE: 1
52 gaattcgaaa cg atg cgt ctg ctg tct acc ttc act gaa tac atc aag aac  51
53                 Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
54                  1               5                  10
56 atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg  99
57 Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
58      15                  20                  25
60 atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt  147
61 Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
62   30                  35                  40                  45
64 aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa  195
65 Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
66                  50                  55                  60
68 tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct  243
```

Does Not Comply
Corrected Diskette Needed

Invalid response 213

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

```
69 Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
70             65                  70                  75
72 atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac   291
73 Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
74             80                  85                  90
76 ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg   339
77 Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
78        95                  100                 105
80 gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc   387
81 Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
82 110                 115                 120                 125
84 tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa   435
85 Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
86             130                 135                 140
88 tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc   483
89 Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
90             145                 150                 155
92 gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac   531
93 Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
94             160                 165                 170
96 ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac   579
97 Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
98        175                 180                 185
100 gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac   627
101 Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
102 190                 195                 200                 205
104 cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac   675
105 Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
106             210                 215                 220
108 gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc   723
109 Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
110             225                 230                 235
112 ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac   771
113 Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr
114             240                 245                 250
116 atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta   819
117 Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
118        255                 260                 265
120 ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg   867
121 Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
122 270                 275                 280                 285
124 act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc   915
125 Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
126             290                 295                 300
128 atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac   963
129 Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
130             305                 310                 315
132 aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt  1011
133 Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
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RAW SEQUENCE LISTING   DATE: 08/06/2001
PATENT APPLICATION: US/09/910,186   TIME: 15:39:04

Input Set : A:\A33626Aseqlist.txt
Output Set: N:\CRF3\08062001\I910186.raw

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134        320                 325                 330
136 ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct   1059
137 Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
138        335                 340                 345
140 ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa   1107
141 Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
142 350                 355                 360                 365
144 tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag   1155
145 Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
146                370                 375                 380
148 gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac   1203
149 Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
150                385                 390                 395
152 aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa   1251
153 Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
154        400                 405                 410
156 cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat   1299
157 Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
158        415                 420                 425
160 gac ggt tgg ggt gaa cgt ccg ctg taa gaattc                        1332
161 Asp Gly Trp Gly Glu Arg Pro Leu  *
162 430                 435
165 <210> SEQ ID NO: 2
166 <211> LENGTH: 437
167 <212> TYPE: PRT
168 <213> ORGANISM: Synthetic Construct
170 <220> FEATURE:
173 <400> SEQUENCE: 2
174 Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
175 1               5                   10                  15
176 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
177            20                  25                  30
178 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
179            35                  40                  45
180 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
181     50                  55                  60
182 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
183 65                  70                  75                  80
184 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
185            85                  90                  95
186 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
187            100                 105                 110
188 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
189            115                 120                 125
190 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
191     130                 135                 140
192 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
193 145                 150                 155                 160
194 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
```

Invalid response 213

```
195                   165                 170                 175
196 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
197               180              . 185               190
198 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
199           195                 200                 205
200 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
201       210                 215                 220
202 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
203 225               230                 235                 240
204 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
205               245                 250        .          255
206 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
207           260                 265                 270
208 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
209           275                 280                 285
210 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
211       290                 295                 300
212 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
213 305               310                 315                 320
214 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
215               325                 330                 335
216 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
217           340                 345                 350
218 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
219           355                 360                 365
220 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
221       370                 375                 380
222 Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
223 385               390                 395                 400
224 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
225               405                 410                 415
226 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
227           420                 425                 430   .
228 Gly Glu Arg Pro Leu
229           435
232 <210> SEQ ID NO: 3
233 <211> LENGTH: 1323
234 <212> TYPE: DNA
235 <213> ORGANISM: Synthetic Construct
237 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (13)...(1314)
242 <223> OTHER INFORMATION: Synthetic Construct
244 <400> SEQUENCE: 3
245 gaattcgaaa cg atg tct acc ttc act gaa tac atc aag aac atc atc aat 51
246               Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
247                1                5                   10
249 acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg   99
250 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
```

```
251      15                    20                      25
253 tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat   147
254 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
255   30                    35                      40                    45
257 ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa   195
258 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
259                    50                      55                      60
261 atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa   243.
262 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
263            65                      70                      75
265 aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc   291
266 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
267            80                      85                      90
269 atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat   339
270 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
271        95                      100                     105
273 tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg   387
274 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
275 110                    115                     120                   125
277 cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag   435
278 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
279-                   130                     135                   140
281 atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc   483
282 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
283            145                     150                     155
285 acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg   531
286 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
287            160                     165                     170
289 atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat   579
290 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
291      175                     180                     185
293 aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc   627
294 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
295 190                    195                     200                   205
297 tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa   675
298 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
299                    210                     215                   220
301 atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac   723
302 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
303            225                     230                     235
305 ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat   771
306 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
307            240                     245                     250
309 ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc   819
310 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
311      255                     260                     265
313 ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac   867
314 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
315 270                    275                     280                   285
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VERIFICATION SUMMARY   DATE: 08/06/2001
PATENT APPLICATION: **US/09/910,186**   TIME: 15:39:05

Input Set : **A:\A33626Aseqlist.txt**
Output Set: **N:\CRF3\08062001\I910186.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date